



IFWO

RAW SEQUENCE LISTING

DATE: 10/13/2004

PATENT APPLICATION: US/10/780,002

TIME: 10:02:28

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\10132004\J780002.raw

4 <110> APPLICANT: Klessig, Daniel F.
 5 Kumar, Dhirenda
 7 <120> TITLE OF INVENTION: NOVEL SALICYLIC ACID-BINDING PROTEIN
 8 ENCODING NUCLEIC ACIDS, SABP2, AND METHODS OF USE THEREOF
 11 <130> FILE REFERENCE: 3670-PO2652WO
 13 <140> CURRENT APPLICATION NUMBER: 10/780,002
 14 <141> CURRENT FILING DATE: 2004-02-17
 17 <150> PRIOR APPLICATION NUMBER: PCT/US02/26312
 18 <151> PRIOR FILING DATE: 2002-08-16
 20 <150> PRIOR APPLICATION NUMBER: 60/312,863
 21 <151> PRIOR FILING DATE: 2001-08-16
 23 <160> NUMBER OF SEQ ID NOS: 58
 25 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 1079
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Nicotiana tabacum
 32 <400> SEQUENCE: 1

(Pg. 6)

ENTERED

33	acgcgggggaa agaaaagaaa ctaacaaggc ataaaattca aatgaaggaa ggaaaacact	60
34	ttgttttagt acatggtgca tgccatggag gttggagttg gtacaagcta aagccactgc	120
35	tagaagctgc aggccataag gttacagccc ttgatttagc agcttctggc actgatttga	180
36	gaaaaataga ggagcttcgc acactttatg attatacttt gccattgatg gagttgatgg	240
37	aatctctttc agcagatgag aagggttatat tagtggggca tagtcttggt ggtatgaatt	300
38	tgggacttgc tatggaaaag tatccacaaa agatctatgc tgetgttttc ttggetgctt	360
39	tcatgcctga ttctgttcac aactctcctt ttgttttggg acagtataat gagcggacgc	420
40	cagccgagaa ttggttggat actcagtttt taccatatgg tccccgtgaa gagccactga	480
41	catccatgtt ttttgGCCa aagttcttgg ctccacaagct ctaccagcta tgctctcctg	540
42	aggatcttgc attagcatca tcattggtga gaccaagctc tttgtttatg gaagacctat	600
43	cgaaggccaa gtatttcaca gatgaacggt ttggatcagt gaagagagtt tacatttgtt	660
44	gcactgagga taaaggcata ccagaagaat tccagcgatg gcaaattgac aacattggtg	720
45	tcactgaagc aatagagatt aaagggtgctg atcacatggc aatgctatgc gagcccaaaa	780
46	aactttgcgc ctctctcttg gaaattgccc ataaatacaa ctgatctcta cattatgtct	840
47	tcgtctcatg tcaagatttt cagtgcagtc tgtaattttt ttctattttt cgaccggcgc	900
48	ataactgtct ttgcctattt taaggattgc agtaatttca ctcttctagt gtggaaggct	960
49	tccacataag gattgttctg tttctccatt caagtgtgtg ttatgttgag atacttaaac	1020
50	cgtatcaatt cttgtaatga aacttcttct ttcctttttg aaaaaaaaaa aaaaaaaaaa	1079

52 <210> SEQ ID NO: 2

53 <211> LENGTH: 260

54 <212> TYPE: PRT

55 <213> ORGANISM: Nicotiana tabacum

57 <400> SEQUENCE: 2

58 Met Lys Glu Gly Lys His Phe Val Leu Val His Gly Ala Cys His Gly

59 1

5

10

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```

60 Gly Trp Ser Trp Tyr Lys Leu Lys Pro Leu Leu Glu Ala Ala Gly His
61          20          25          30
62 Lys Val Thr Ala Leu Asp Leu Ala Ala Ser Gly Thr Asp Leu Arg Lys
63          35          40          45
64 Ile Glu Glu Leu Arg Thr Leu Tyr Asp Tyr Thr Leu Pro Leu Met Glu
65          50          55          60
66 Leu Met Glu Ser Leu Ser Ala Asp Glu Lys Val Ile Leu Val Gly His
67 65          70          75          80
68 Ser Leu Gly Gly Met Asn Leu Gly Leu Ala Met Glu Lys Tyr Pro Gln
69          85          90          95
70 Lys Ile Tyr Ala Ala Val Phe Leu Ala Ala Phe Met Pro Asp Ser Val
71          100         105         110
72 His Asn Ser Ser Phe Val Leu Glu Gln Tyr Asn Glu Arg Thr Pro Ala
73          115         120         125
74 Glu Asn Trp Leu Asp Thr Gln Phe Leu Pro Tyr Gly Ser Pro Glu Glu
75          130         135         140
76 Pro Leu Thr Ser Met Phe Phe Gly Pro Lys Phe Leu Ala His Lys Leu
77 145          150          155          160
78 Tyr Gln Leu Cys Ser Pro Glu Asp Leu Ala Leu Ala Ser Ser Leu Val
79          165          170          175
80 Arg Pro Ser Ser Leu Phe Met Glu Asp Leu Ser Lys Ala Lys Tyr Phe
81          180          185          190
82 Thr Asp Glu Arg Phe Gly Ser Val Lys Arg Val Tyr Ile Val Cys Thr
83          195          200          205
84 Glu Asp Lys Gly Ile Pro Glu Glu Phe Gln Arg Trp Gln Ile Asp Asn
85          210          215          220
86 Ile Gly Val Thr Glu Ala Ile Glu Ile Lys Gly Ala Asp His Met Ala
87 225          230          235          240
88 Met Leu Cys Glu Pro Gln Lys Leu Cys Ala Ser Leu Leu Glu Ile Ala
89          245          250          255
90 His Lys Tyr Asn
91          260
93 <210> SEQ ID NO: 3
94 <211> LENGTH: 258
95 <212> TYPE: PRT
96 <213> ORGANISM: Manihot esculenta
98 <400> SEQUENCE: 3
99 Met Ala Val Val Asp Phe Val Leu Ile His Thr Ile Cys His Gly Ala
100 1          5          10          15
101 Trp Ile Trp Tyr Lys Leu Lys Pro Val Leu Glu Ala Ala Gly His Lys
102          20          25          30
103 Val Thr Ala Leu Asp Leu Ala Ala Ser Gly Val Asp Pro Arg Gln Ile
104          35          40          45
105 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
106          50          55          60
107 Met Glu Ser Leu Pro Gln Gly Glu Lys Val Ile Leu Val Gly Glu Ser
108 65          70          75          80
109 Cys Gly Gly Leu Asn Ile Ala Ile Ala Ala Asp Lys Tyr Pro Glu Lys
110          85          90          95

```

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```

111 Ile Ala Ala Ala Val Phe Gln Asn Ser Leu Leu Pro Asp Thr Lys His
112           100           105           110
113 Lys Pro Ser Tyr Val Val Asp Lys Leu Met Glu Val Phe Pro Asp Trp
114           115           120           125
115 Lys Asp Thr Glu Tyr Phe Glu Phe Ser Asn Ser Asn Gly Glu Thr Ile
116           130           135           140
117 Thr Gly Met Val Leu Gly Leu Lys Leu Met Arg Glu Asn Leu Tyr Thr
118           145           150           155           160
119 Ile Cys Pro Pro Glu Asp Tyr Glu Leu Ala Lys Met Leu Thr Arg Arg
120           165           170           175
121 Gly Ser Leu Phe Gln Ser Ile Leu Ala Gln Arg Glu Lys Phe Thr Glu
122           180           185           190
123 Lys Gly Tyr Gly Ser Ile Lys Lys Ile Tyr Val Trp Thr Gly Asp Asp
124           195           200           205
125 Lys Ile Phe Leu Pro Glu Phe Gln Leu Trp Gln Ile Glu Asn Tyr Lys
126           210           215           220
127 Pro Asp Leu Val Phe Arg Val Met Gly Gly Asp His Lys Leu Gln Leu
128           225           230           235           240
129 Thr Lys Thr Asn Glu Ile Ala Gly Ile Leu Gln Lys Val Ala Asp Ile
130           245           250           255
131 Tyr Ala
134 <210> SEQ ID NO: 4
135 <211> LENGTH: 257
136 <212> TYPE: PRT
137 <213> ORGANISM: Hevea brasiliensis
139 <400> SEQUENCE: 4
140 Met Ala Phe Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
141   1           5           10           15
142 Trp Ile Trp His Lys Leu Lys Pro Leu Leu Glu Ala Leu Gly His Lys
143           20           25           30
144 Val Thr Ala Leu Asp Leu Ala Ala Ser Gly Val Asp Pro Arg Gln Ile
145           35           40           45
146 Glu Glu Ile Gly Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
147           50           55           60
148 Leu Glu Ala Leu Pro Pro Gly Glu Lys Val Ile Leu Val Gly Glu Ser
149           65           70           75           80
150 Cys Gly Gly Leu Asn Ile Ala Ile Ala Ala Asp Lys Tyr Cys Glu Lys
151           85           90           95
152 Ile Ala Ala Ala Val Phe His Asn Ser Val Leu Pro Asp Thr Glu His
153           100           105           110
154 Cys Pro Ser Tyr Val Val Asp Lys Leu Met Glu Val Phe Pro Asp Trp
155           115           120           125
156 Lys Asp Thr Thr Tyr Phe Thr Tyr Thr Lys Asp Gly Lys Glu Ile Thr
157           130           135           140
158 Gly Leu Lys Leu Gly Phe Thr Leu Leu Arg Glu Asn Leu Tyr Thr Leu
159           145           150           155           160
160 Cys Gly Pro Glu Glu Tyr Glu Leu Ala Lys Met Leu Thr Arg Lys Gly
161           165           170           175
162 Ser Leu Phe Gln Asn Ile Leu Ala Lys Arg Pro Phe Phe Thr Lys Glu

```

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```

163          180          185          190
164 Gly Tyr Gly Ser Ile Lys Lys Ile Tyr Val Trp Thr Asp Gln Asp Glu
165          195          200          205
166 Ile Phe Leu Pro Glu Phe Gln Leu Trp Gln Ile Glu Asn Tyr Lys Pro
167          210          215          220
168 Asp Lys Val Tyr Lys Val Glu Gly Gly Asp His Lys Leu Gln Leu Thr
169 225          230          235          240
170 Lys Thr Lys Glu Ile Ala Glu Ile Leu Gln Glu Val Ala Asp Thr Tyr
171          245          250          255
172 Asn
175 <210> SEQ ID NO: 5
176 <211> LENGTH: 263
177 <212> TYPE: PRT
178 <213> ORGANISM: Arabidopsis thaliana
180 <400> SEQUENCE: 5
181 Met Ser Glu Glu Lys Arg Lys Gln His Phe Val Leu Val His Gly Ser
182 1          5          10          15
183 Cys His Gly Ala Trp Cys Trp Tyr Lys Val Lys Pro Leu Leu Glu Ala
184          20          25          30
185 Val Gly His Arg Val Thr Ala Val Asp Leu Ala Ala Ser Gly Ile Asp
186          35          40          45
187 Thr Thr Arg Ser Ile Thr Asp Ile Pro Thr Cys Glu Gln Tyr Ser Glu
188          50          55          60
189 Pro Leu Thr Lys Leu Leu Thr Ser Leu Pro Asn Asp Glu Lys Val Val
190 65          70          75          80
191 Leu Val Gly His Ser Phe Gly Gly Leu Asn Leu Ala Ile Ala Met Glu
192          85          90          95
193 Lys Phe Pro Glu Lys Ile Ser Val Ala Val Phe Leu Thr Ala Phe Met
194          100          105          110
195 Pro Asp Thr Glu His Ser Pro Ser Phe Val Leu Asp Lys Phe Gly Ser
196          115          120          125
197 Asn Met Pro Gln Glu Ala Trp Met Gly Thr Glu Phe Glu Pro Tyr Gly
198          130          135          140
199 Ser Asp Asn Ser Gly Leu Ser Met Phe Phe Ser Pro Asp Phe Met Lys
200 145          150          155          160
201 Leu Gly Leu Tyr Gln Leu Ser Pro Val Glu Asp Leu Glu Leu Gly Leu
202          165          170          175
203 Leu Leu Met Arg Pro Gly Ser Leu Phe Ile Asn Asp Leu Ser Lys Met
204          180          185          190
205 Lys Asn Phe Ser Asp Glu Gly Tyr Gly Ser Val Pro Arg Val Phe Ile
206          195          200          205
207 Val Cys Lys Glu Asp Lys Ala Ile Pro Glu Glu Arg Gln Arg Trp Met
208          210          215          220
209 Ile Asp Asn Phe Pro Val Asn Leu Val Met Glu Met Glu Glu Thr Asp
210 225          230          235          240
211 His Met Pro Met Phe Cys Lys Pro Gln Gln Leu Ser Asp Tyr Phe Leu
212          245          250          255
213 Lys Ile Ala Asp Lys Phe Val
214          260

```

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```

216 <210> SEQ ID NO: 6
217 <211> LENGTH: 268
218 <212> TYPE: PRT
219 <213> ORGANISM: Rice
221 <400> SEQUENCE: 6
222 Met Glu Ile Ser Ser Ser Ser Lys Lys His Phe Ile Leu Val His Gly
223   1           5           10           15
224 Leu Cys His Gly Ala Trp Cys Trp Tyr Arg Val Val Ala Ala Leu Arg
225           20           25           30
226 Ala Ala Gly His Arg Ala Thr Ala Leu Asp Met Ala Ala Ser Gly Ala
227           35           40           45
228 His Pro Ala Arg Val Asp Glu Val Gly Thr Phe Glu Glu Tyr Ser Arg
229           50           55           60
230 Pro Leu Leu Asp Ala Val Ala Ala Ala Ala Ala Pro Gly Glu Arg Leu
231           65           70           75           80
232 Val Leu Val Gly His Ser His Gly Gly Leu Ser Val Ala Leu Ala Met
233           85           90           95
234 Glu Arg Phe Pro Asp Lys Val Ala Ala Ala Val Phe Val Ala Ala Ala
235           100          105          110
236 Met Pro Cys Val Gly Lys His Met Gly Val Pro Thr Glu Glu Phe Met
237           115          120          125
238 Arg Arg Thr Ala Pro Glu Gly Leu Leu Met Asp Cys Glu Met Val Ala
239           130          135          140
240 Ile Asn Asn Ser Gln Gly Ser Gly Val Ala Ile Asn Leu Gly Pro Thr
241           145          150          155          160
242 Phe Leu Ala Gln Lys Tyr Tyr Gln Gln Ser Pro Ala Glu Asp Leu Ala
243           165          170          175
244 Leu Ala Lys Met Leu Val Arg Pro Gly Asn Gln Phe Met Asp Asp Pro
245           180          185          190
246 Val Met Lys Asp Glu Ser Leu Leu Thr Asn Gly Asn Tyr Gly Ser Val
247           195          200          205
248 Lys Lys Val Tyr Val Ile Ala Lys Ala Asp Ser Ser Ser Thr Glu Glu
249           210          215          220
250 Met Gln Arg Trp Met Val Ala Met Ser Pro Gly Thr Asp Val Glu Glu
251           225          230          235          240
252 Ile Ala Gly Ala Asp His Ala Val Met Asn Ser Lys Pro Arg Glu Leu
253           245          250          255
254 Cys Asp Ile Leu Ile Lys Ile Ala Asn Lys Tyr Glu
255           260          265

```

```

257 <210> SEQ ID NO: 7
258 <211> LENGTH: 20
259 <212> TYPE: DNA
260 <213> ORGANISM: Artificial Sequence
262 <220> FEATURE:

```

```

263 <223> OTHER INFORMATION: primer

```

```

W--> 265 <221> NAME/KEY: variation

```

```

266 <222> LOCATION: (0)...(0)

```

```

267 <223> OTHER INFORMATION: n at position 3 is a or t, n at position 6 is a or

```

```

268      g, n at position 9 is c or t, n at position 12 is

```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/780,002

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Input Set : A:\SEQUENCE LISTING.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; N Pos. 3, 6, 9, 12, 15, 18
Seq#:12; Xaa Pos. 1
Seq#:13; Xaa Pos. 2
Seq#:14; Xaa Pos. 6
Seq#:15; Xaa Pos. 11, 13
Seq#:16; Xaa Pos. 1
Seq#:17; Xaa Pos. 4, 6, 8
Seq#:19; Xaa Pos. 2
Seq#:22; Xaa Pos. 1
Seq#:23; Xaa Pos. 1, 2, 8, 9
Seq#:25; Xaa Pos. 1, 6, 7
Seq#:29; Xaa Pos. 3
Seq#:30; Xaa Pos. 2, 4

VERIFICATION SUMMARY

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Input Set : A:\SEQUENCE LISTING.txt

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L:265 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:272 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:329 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:406 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:411 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:468 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
L:487 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23
L:492 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23
L:497 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23
L:498 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0
L:526 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:25
L:531 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:25
L:532 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
L:573 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0
L:587 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0